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genetic correlation, and, as noted above, development of the theory for understanding the genetics of complex human diseases in terms of an underlying continuous liability.

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they morphological or
physiological
characters, aspects of
behavior, or genome-

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which many genes influence the trait and in which non-genetic factors may also be important. Evolution and Selection of Quantitative Traits presents a holistic treatment of the subject, showing the interplay between theory and data with extensive discussions on statistical issues relating to the

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on which methods may
be most appropriate for
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sections. The first
section (Chapters 1 to 8)
covers topics of
classical phenotypic
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programs. In the second section (Chapters 9 to 13) we provide the concept and overall review of available tools for using DNA markers for predictions of genetic merits in breeding populations. With advances in DNA sequencing technologies, genomic data, especially single nucleotide

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polymorphism (SNP) markers, have become available for animal and plant breeding programs in recent years. Analysis of DNA markers for prediction of genetic merit is a relatively new and active research area. The algorithms and software to implement these algorithms are changing rapidly. This section represents state-

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